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☐ 1. Document ID: US 20030148263 A1

L9: Entry 1 of 2 File: PGPB Aug 7, 2003

DOCUMENT-IDENTIFIER: US 20030148263 A1
TITLE: Methods and compositions using genetic package display

Summary of Invention Paragraph:
[0010] However, the ability to recover the most useful cell binding ligands rapidly is extremely limited. In theory, if it were possible to incubate a phage library with a target for sufficient time with efficient washing away of non-binders, while leaving binders intact such that they can be recovered as infective phage, then one would be able to isolate a relatively pure population of binding phage in a single round of selection. However, this is rarely the case, and even the relatively simple selection of binding phage against a purified molecular target requires several rounds to "affinity purify" the desired phage. Selection against more complex targets, such as whole cells, can take six or more rounds of selection, and this is only for detecting ligands that bind, excluding internalization. There are several possible explanations for why several rounds of screening are necessary, one being the problem of background. Even so-called non-binders have a certain affinity for the target (or the solid support, cell surface, etc.). Since non-binders are commonly in million fold or more excess, even low affinity binders will result in a background of false positives. On the other hand, true binders of modest affinity may be lost if washes are too stringent, and tight binders could be lost if they can not be removed from the target or if removal results in loss of infectivity.

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw D

☐ 2. Document ID: US 6972183 B1

L9: Entry 2 of 2 File: USPT Dec 6, 2005

DOCUMENT-IDENTIFIER: US 6972183 B1
TITLE: Capillary array-based enzyme screening

Detailed Description Text (4):
The present invention permits the rapid screening of complex environmental expression libraries, representing, for example, thousands of different organisms. The analysis of a complex sample of this size requires one to screen up to several million clones to cover this genomic biodiversity. The present invention provides a high-throughput capillary array-based screening method that allows one to assess

this enormous number of clones to identify and recover cells encoding useful enzymes, as well as other biomolecules (particularly ligands). While the preferred embodiments relate primarily to enzymes having a desired enzyme, activity, the present invention is also useful with regard to other biomolecules having a desired biological activity. In particular, the capillary array-based techniques described herein can be used to screen, identify and recover proteins having a desired bioactivity or other ligands having a desired binding affinity. For example, binding assays may be conducted by using an appropriate substrate or other marker that emits a detectable signal upon the occurrence of the desired binding event. Many of the substrates discussed below, as well as numerous markers known in the art, are suitable for such binding assays.

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Terms	Documents
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